

## **RAW SEQUENCE LISTING**

**Loaded by SCORE, no errors detected.**

Application Serial Number: **10609296**

Source: **OIPE**

Date Processed by SCORE: **9/16/2008**

***ENTERED***

<110> APPLICANT: RASMUSSEN, Poul Baad  
DRUSTRUP, Jorn  
RASMUSSEN, Grethe  
PEDERSEN, Anders Hjelholt  
SCHAMBYE, Hans Thalsg+rd  
ANDERSEN, Kim Vilbour  
BORNS, Claus  
Maxygen ApS  
Maxygen Holdings Ltd.  
<120> TITLE OF INVENTION: NEW INTERFERON BETA-LIKE MOLECULES  
<130> FILE REFERENCE: 0228us410

<140> CURRENT APPLICATION NUMBER: 10609296  
<141> CURRENT FILING DATE: 2003-06-27  
<150> PRIOR APPLICATION NUMBER: US/10/084,706  
<151> PRIOR FILING DATE: 2002-02-26  
<150> PRIOR APPLICATION NUMBER: US 60/272,116  
<151> PRIOR FILING DATE: 2001-02-27  
<150> PRIOR APPLICATION NUMBER: US 60/343,436  
<151> PRIOR FILING DATE: 2001-12-21  
<150> PRIOR APPLICATION NUMBER: US 60/302,140  
<151> PRIOR FILING DATE: 2001-06-29  
<150> PRIOR APPLICATION NUMBER: US 60/316,170  
<151> PRIOR FILING DATE: 2001-08-30  
<150> PRIOR APPLICATION NUMBER: not yet assigned  
<151> PRIOR FILING DATE: 2002-02-19  
<150> PRIOR APPLICATION NUMBER: DK PA 2001 00333  
<151> PRIOR FILING DATE: 2001-03-01  
<150> PRIOR APPLICATION NUMBER: US 09/648,569  
<151> PRIOR FILING DATE: 2000-08-25  
<160> NUMBER OF SEQ ID NOS: 57  
<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1  
<211> LENGTH: 840  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (76)...(636)  
<400> SEQUENCE: 1  
acattctaac tgcaacccttt cgaaggcctt gctctggcac aacaggttgtt aggccacact  
60  
gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg  
111  
159  
207  
255  
303

111  
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu  
1 5 10  
ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga  
159  
Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly  
15 20 25  
ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa  
207  
Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln  
30 35 40  
ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac  
255  
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp  
45 50 55 60  
atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc

Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala  
                      65                     70                     75  
 gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga  
 351 Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg  
                      80                     85                     90  
 caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc  
 399 Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu  
                      95                     100                    105  
 ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa  
 447 Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu  
                      110                    115                    120  
 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt  
 495 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser  
                      125                    130                    135                    140  
 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc  
 543 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala  
                      145                    150                    155  
 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta  
 591 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu  
                      160                    165                    170  
 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac  
 636 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
                      175                    180                    185  
 tgaagatctc ctggctgtg cctctggac tggacaattt cttcaagcat tcttcaacca  
 696 gcagatgttg ttaagtgtac tgatggctaa tgtactgtcat atgaaaggac actagaagat  
 756 tttgaaattt ttatcaaattt atgagttatt ttatatttatt taaattttat ttggaaaat  
 816 aaattatttt tggcAAAAA gtca  
 840

<210> SEQ\_ID NO 2  
 <211> LENGTH: 166  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <220> FEATURE:  
 <221> NAME/KEY: CHAIN  
 <222> LOCATION: (1)...(166)  
 <223> OTHER INFORMATION: hIFNB mature sequence  
 <400> SEQUENCE: 2  
 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
   1                     5                     10                     15  
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu  
   20                    25                    30  
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln  
   35                    40                    45  
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
   50                    55                    60  
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
   65                    70                    75                    80  
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
   85                    90                    95  
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Asp Phe Thr

	100	105	110												
Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
			115					120				125			
Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
			130			135				140					
Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu
	145			150					155				160		
Thr	Gly	Tyr	Leu	Arg	Asn										
			165												

<210> SEQ ID NO 3  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 3  
60       ggctagcggt taaacttaag cttcgccacc atgaccaaca agtgccctgct ccagatcgcc  
70       ctgctcctgt

<210> SEQ ID NO 4  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 4  
60       acaacctgct cggcttcctg cagaggagtt cgaacttcca gtgccagaag ctcctgtggc  
70       agctgaacgg

<210> SEQ ID NO 5  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 5  
60       gaacttcgac atccccgagg aaatcaagca gctgcagcag ttccagaagg aggacgcccgc  
70       tctgaccatc

<210> SEQ ID NO 6  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 6  
60       ttccgccagg actccagctc caccgggtgg aacgagacca tcgtggagaa cctgctggcc  
70       aacgtgtacc

<210> SEQ ID NO 7  
<211> LENGTH: 70  
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 7  
      aggagaagct ggagaaggag gacttcaccc gcggcaagct gatgagctcc ctgcacctga  
60  
      agcgctacta  
70

<210> SEQ ID NO 8  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 8  
      ggagtagacgc cactgcgcct ggaccatcgt acgcgtggag atcctgcgca acttctactt  
60  
      catcaaccgc  
70

<210> SEQ ID NO 9  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 9  
      caccacactg gactagtgga tccttatcag ttgcgcaggt agccggtcag gcggttgatg  
60  
      aagtagaagt  
70

<210> SEQ ID NO 10  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 10  
      aggcgcagtg gctgtactcc ttggccttca ggtagtgcag gatgcggcca tagtagcgct  
60  
      tcaggtgcag  
70

<210> SEQ ID NO 11  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 11  
      ctccttctcc agcttctccct ccagcacggc ctccaggtgg ttgatctgg ggtacacggt  
60  
      ggccagcagg  
70

<210> SEQ ID NO 12  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 12  
60       gagctggagt cctggcggaa gatggcgaag atgttctgca gcatctcgta gatggtcaga  
70       gcggcggtcct

<210> SEQ ID NO 13  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 13  
60       cctcggggat gtcgaagttc atcctgtcct tcaggcagta ctccaggcgc ccgttcagct  
70       gccacaggag

<210> SEQ ID NO 14  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 14  
60       caggaagccg agcaggttgt agctcatcga tagggccgtg gtgctgaagc acaggagcag  
70       ggcgatctgg

<210> SEQ ID NO 15  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 15  
60       ctgctccaga tcgcccgtct cctgtgtttc agcaccacgg ccctatcgat gaagcaccag  
70       caccagcatc

<210> SEQ ID NO 16  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 16  
60       cactgcttac tggcttatcg aaattaatac gactcactat agggagaccc aagctggcta  
70       gcgtttaaac

<210> SEQ ID NO 17  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE: